

## SEQUENCE LISTING

<110> Glucksmann, Maria A.  
Kadambi, Vivek

<120> 33358, A NOVEL HUMAN ANKYRIN FAMILY MEMBER AND USES THEREOF

<130> MNI-162CP

<150> 60/212,222

<151> 2000-06-16

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<211> 1538

<212> DNA

<213> Homo sapiens

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<221> CDS

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att ttt att aca atg ttt gct acg ttt ttt ttc ttt aag ctt tta att 158
Ile Phe Ile Thr Met Phe Ala Thr Phe Phe Phe Phe Lys Leu Leu Ile
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aaa gtt ttt ttg gct ctc cta acc cat ttc tat atc gtc aaa gga aat 206
Lys Val Phe Leu Ala Leu Leu Thr His Phe Tyr Ile Val Lys Gly Asn
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aga aaa gaa gcg gct agg ata gca gaa gag atc tat ggt gga att tca 254
Arg Lys Glu Ala Ala Arg Ile Ala Glu Glu Ile Tyr Gly Gly Ile Ser
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gat tgc tgg gct gat cga tcc oca ctt cat gaa gct gca gct cag ggg 302
Asp Cys Trp Ala Asp Arg Ser Pro Leu His Glu Ala Ala Ala Gln Gly
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cgc tta ctg gcc ctt aaa act tta att gca caa ggt gtc aat gtg aac 350
Arg Leu Leu Ala Leu Lys Thr Leu Ile Ala Gln Gly Val Asn Val Asn
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ctt gtg aca att aac cgg gtg tct tct ctc cac gag gca tgc ctt gga 398
Leu Val Thr Ile Asn Arg Val Ser Ser Leu His Glu Ala Cys Leu Gly
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09884370-061301

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 Gly His Val Ala Cys Ala Lys Ala Leu Leu Glu Asn Gly Ala His Val  
 110 115 120

aat gga gtg aca gtt cac gga gcc aca ccc ctc ttc aat gct tgc tgc 494  
 Asn Gly Val Thr Val His Gly Ala Thr Pro Leu Phe Asn Ala Cys Cys  
 125 130 135 140

agc ggc agt gct gca tgt gtc aat gtg ctg ctg gag ttc gga gcc aag 542  
 Ser Gly Ser Ala Ala Cys Val Asn Val Leu Leu Glu Phe Gly Ala Lys  
 145 150 155

gcc cag ttg gag gtg cac ctg gcc tcg ccc atc cat gag gca gtg aag 590  
 Ala Gln Leu Glu Val His Leu Ala Ser Pro Ile His Glu Ala Val Lys  
 160 165 170

aga ggt cac aga gag tgc atg gag atc ctg ctg gca aat aat gtt aac 638  
 Arg Gly His Arg Glu Cys Met Glu Ile Leu Leu Ala Asn Asn Val Asn  
 175 180 185

att gac cat gag gtg cct cag ctc gga act ccc cta tat gtg gcc tgc 686  
 Ile Asp His Glu Val Pro Gln Leu Gly Thr Pro Leu Tyr Val Ala Cys  
 190 195 200

acc tac cag agg gta gac tgt gtg aag aaa ctt cta gaa tta gga gcc 734  
 Thr Tyr Gln Arg Val Asp Cys Val Lys Lys Leu Leu Glu Leu Gly Ala  
 205 210 215 220

agt gtc gac cat ggc cag tgg ctg gac acc cca ctc cat gct gca gcg 782  
 Ser Val Asp His Gly Gln Trp Leu Asp Thr Pro Leu His Ala Ala Ala  
 225 230 235

agg cag tcc aat gtg gag gtc atc cac ctg cta acc gac tat gga gct 830  
 Arg Gln Ser Asn Val Glu Val Ile His Leu Leu Thr Asp Tyr Gly Ala  
 240 245 250

aac ctg aag cgt aga aat gct cag ggc aaa agt gcg ctt gat ctg gcg 878  
 Asn Leu Lys Arg Arg Asn Ala Gln Gly Lys Ser Ala Leu Asp Leu Ala  
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gct cca aaa agc agc gtg gag cag gca ctc ttg ctc cgt gaa ggc cca 926  
 Ala Pro Lys Ser Ser Val Glu Gln Ala Leu Leu Leu Arg Glu Gly Pro  
 270 275 280

cct gct ctt tcc cag ctc tgc cgc ctg tgt gtc cgg aag tgt ctc ggt 974  
 Pro Ala Leu Ser Gln Leu Cys Arg Leu Cys Val Arg Lys Cys Leu Gly  
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cga gca tgt cat caa gcc atc cac aag cta cat ctg cca gag cca ctc 1022  
 Arg Ala Cys His Gln Ala Ile His Lys Leu His Leu Pro Glu Pro Leu  
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gaa cga ttc ctc cta tac caa tag tcctaagtgt tcctgggaag atacttgga 1076  
 Glu Arg Phe Leu Leu Tyr Gln \*  
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0564370-051801

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Ala Arg Ile Ala Glu Glu Ile Tyr Gly Gly Ile Ser Asp Cys Trp Ala
50     55     60
Asp Arg Ser Pro Leu His Glu Ala Ala Ala Gln Gly Arg Leu Leu Ala
65     70     75     80
Leu Lys Thr Leu Ile Ala Gln Gly Val Asn Val Asn Leu Val Thr Ile
85     90     95
Asn Arg Val Ser Ser Leu His Glu Ala Cys Leu Gly Gly His Val Ala
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Cys Ala Lys Ala Leu Leu Glu Asn Gly Ala His Val Asn Gly Val Thr
115    120    125
Val His Gly Ala Thr Pro Leu Phe Asn Ala Cys Cys Ser Gly Ser Ala
130    135    140
Ala Cys Val Asn Val Leu Leu Glu Phe Gly Ala Lys Ala Gln Leu Glu
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Val His Leu Ala Ser Pro Ile His Glu Ala Val Lys Arg Gly His Arg
165    170    175
Glu Cys Met Glu Ile Leu Leu Ala Asn Asn Val Asn Ile Asp His Glu
180    185    190
Val Pro Gln Leu Gly Thr Pro Leu Tyr Val Ala Cys Thr Tyr Gln Arg
195    200    205
Val Asp Cys Val Lys Lys Leu Leu Glu Leu Gly Ala Ser Val Asp His
210    215    220
Gly Gln Trp Leu Asp Thr Pro Leu His Ala Ala Arg Gln Ser Asn
225    230    235    240
Val Glu Val Ile His Leu Leu Thr Asp Tyr Gly Ala Asn Leu Lys Arg
245    250    255
Arg Asn Ala Gln Gly Lys Ser Ala Leu Asp Leu Ala Ala Pro Lys Ser
260    265    270
Ser Val Glu Gln Ala Leu Leu Leu Arg Glu Gly Pro Pro Ala Leu Ser
275    280    285
Gln Leu Cys Arg Leu Cys Val Arg Lys Cys Leu Gly Arg Ala Cys His
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09384870-061301

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gct ctc cta acc cat ttc tat atc gtc aaa gga aat aga aaa gaa gcg 144  
 Ala Leu Leu Thr His Phe Tyr Ile Val Lys Gly Asn Arg Lys Glu Ala  
 35 40 45

gct agg ata gca gaa gag atc tat ggt gga att tca gat tgc tgg gct 192  
 Ala Arg Ile Ala Glu Glu Ile Tyr Gly Gly Ile Ser Asp Cys Trp Ala  
 50 55 60

gat cga tcc cca ctt cat gaa gct gca gct cag ggg cgc tta ctg gcc 240  
 Asp Arg Ser Pro Leu His Glu Ala Ala Ala Gln Gly Arg Leu Leu Ala  
 65 70 75 80

ctt aaa act tta att gca caa ggt gtc aat gtg aac ctt gtg aca att 288  
 Leu Lys Thr Leu Ile Ala Gln Gly Val Asn Val Asn Leu Val Thr Ile  
 85 90 95

aac cgg gtg tct tct ctc cac gag gca tgc ctt gga ggt cac gtg gcc 336  
 Asn Arg Val Ser Ser Leu His Glu Ala Cys Leu Gly Gly His Val Ala  
 100 105 110

tgt gcc aaa gcc tta ttg gaa aat ggt gca cac gtc aat gga gtg aca 384  
 Cys Ala Lys Ala Leu Leu Glu Asn Gly Ala His Val Asn Gly Val Thr  
 115 120 125

gtt cac gga gcc aca ccc ctc ttc aat gct tgc tgc agc ggc agt gct 432  
 Val His Gly Ala Thr Pro Leu Phe Asn Ala Cys Cys Ser Gly Ser Ala  
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 Ala Cys Val Asn Val Leu Leu Glu Phe Gly Ala Lys Ala Gln Leu Glu  
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gtg cac ctg gcc tcg ccc atc cat gag gca gtg aag aga ggt cac aga 528  
 Val His Leu Ala Ser Pro Ile His Glu Ala Val Lys Arg Gly His Arg  
 165 170 175

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05864670-061801

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gta	gac	tgt	gtg	aag	aaa	ctt	cta	gaa	tta	gga	gcc	agt	gtc	gac	cat	672				
Val	Asp	Cys	Val	Lys	Lys	Leu	Leu	Glu	Leu	Gly	Ala	Ser	Val	Asp	His					
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		275					280					285								
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Leu	Tyr	Gln	*																	

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